

1 / 3 2

SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.  
THE UNIVERSITY OF TOKYO

<120> EphA4 as therapeutic target of PRC and PDACa

<130> ONC-A0413P

<150> US 60/548,335

<151> 2004-02-27

<150> US 60/555,809

<151> 2004-03-24

<160> 23

<170> PatentIn version 3.1

<210> 1

<211> 3468

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

2 / 3 2

&lt;222&gt; (43).. (3003)

&lt;223&gt;

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ctgggataga agcggcagga gcagcgttgg caccggcgaa cc atg gct ggg att 54

Met Ala Gly Ile

1

ttc tat ttc gcc cta ttt tcg tgt ctc ttc ggg att tgc gac gct gtc 102

Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys Asp Ala Val

5

10

15

20

aca ggt tcc agg gta tac ccc gcg aat gaa gtt acc tta ttg gat tcc 150

Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr Leu Leu Asp Ser

25

30

35

aga tct gtt cag gga gaa ctt ggg tgg ata gca agc cct ctg gaa gga 198

Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro Leu Glu Gly

40

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ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat aca cca atc cga 246

Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn Thr Pro Ile Arg

55

60

65

acc tac caa gtg tgc aat gtg atg gaa ccc agc cag aat aac tgg cta 294

Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln Asn Asn Trp Leu

3 / 3 2

70	75	80	
cga act gat tgg atc acc cga gaa ggg gct cag agg gtg tat att gag			342
Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile Glu			
85	90	95	100
att aaa ttc acc ttg agg gac tgc aat agt ctt ccg ggc gtc atg ggg			390
Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met Gly			
	105	110	115
act tgc aag gag acg ttt aac ctg tac tac tat gaa tca gac aac gac			438
Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp			
120	125	130	
aaa gag cgt ttc atc aga gag aac cag ttt gtc aaa att gac acc att			486
Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys Ile Asp Thr Ile			
135	140	145	
gct gct gat gag agc ttc acc caa gtg gac att ggt gac aga atc atg			534
Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly Asp Arg Ile Met			
150	155	160	
aag ctg aac acc gag atc cgg gat gta ggg cca tta agc aaa aag ggg			582
Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu Ser Lys Lys Gly			
165	170	175	180

4 / 3 2

ttt tac ctg gct ttt cag gat gtg ggg gcc tgc atc gcc ctg gta tca 630

Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val Ser

185

190

195

gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc cgc aat ctg gcc 678

Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val Arg Asn Leu Ala

200

205

210

cag ttt cct gac acc atc aca ggg gct gat acg tct tcc ctg gtg gaa 726

Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser Ser Leu Val Glu

215

220

225

gtt cga ggc tcc tgt gtc aac aac tca gaa gag aaa gat gtg cca aaa 774

Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys Asp Val Pro Lys

230

235

240

atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc att ggc aac tgc 822

Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro Ile Gly Asn Cys

245

250

255

260

cta tgc aac gct ggg cat gag gag cgg agc gga gaa tgc caa gct tgc 870

Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu Cys Gln Ala Cys

265

270

275

aaa att gga tat tac aag gct ctc tcc acg gat gcc acc tgt gcc aag 918

Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala Thr Cys Ala Lys

5 / 3 2

280	285	290	
tgc cca ccc cac agc tac tct gtc tgg gaa gga gcc acc tcg tgc acc			966
Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala Thr Ser Cys Thr			
295	300	305	
tgt gac cga ggc ttt ttc aga gct gac aac gat gct gcc tct atg ccc			1014
Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala Ala Ser Met Pro			
310	315	320	
tgc acc cgt cca cca tct gct ccc ctg aac ttg att tca aat gtc aac			1062
Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile Ser Asn Val Asn			
325	330	335	340
gag aca tct gtg aac ttg gaa tgg agt agc cct cag aat aca ggt ggc			1110
Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln Asn Thr Gly Gly			
345	350	355	
cgc cag gac att tcc tat aat gtg gta tgc aag aaa tgt gga gct ggt			1158
Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys Cys Gly Ala Gly			
360	365	370	
gac ccc agc aag tgc cga ccc tgt gga agt ggg gtc cac tac acc cca			1206
Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val His Tyr Thr Pro			
375	380	385	

6 / 3 2

cag cag aat ggc ttg aag acc acc aaa gtc tcc atc act gac ctc cta 1254

Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Thr Asp Leu Leu

390

395

400

gct cat acc aat tac acc ttt gaa atc tgg gct gtg aat gga gtg tcc 1302

Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val Asn Gly Val Ser

405

410

415

420

aaa tat aac cct aac cca gac caa tca gtt tct gtc act gtg acc acc 1350

Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val Thr Val Thr Thr

425

430

435

aac caa gca gca cca tca tcc att gct ttg gtc cag gct aaa gaa gtc 1398

Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln Ala Lys Glu Val

440

445

450

aca aga tac agt gtg gca ctg gct tgg ctg gaa cca gat cgg ccc aat 1446

Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro Asp Arg Pro Asn

455

460

465

ggg gta atc ctg gaa tat gaa gtc aag tat tat gag aag gat cag aat 1494

Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn

470

475

480

gag cga agc tat cgt ata gtt cgg aca gct gcc agg aac aca gat atc 1542

Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg Asn Thr Asp Ile

7 / 3 2

485	490	495	500	
aaa ggc ctg aac cct ctc act tcc tat gtt ttc cac gtg cga gcc agg				1590
Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His Val Arg Ala Arg				
	505	510	515	
aca gca gct ggc tat gga gac ttc agt gag ccc ttg gag gtt aca acc				1638
Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu Glu Val Thr Thr				
	520	525	530	
aac aca gtg cct tcc cgg atc att gga gat ggg gct aac tcc aca gtc				1686
Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala Asn Ser Thr Val				
	535	540	545	
ctt ctg gtc tct gtc tcg ggc agt gtg gtg ctg gtg gta att ctc att				1734
Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val Val Ile Leu Ile				
	550	555	560	
gca gct ttt gtc atc agc cgg aga cgg agt aaa tac agt aaa gcc aaa				1782
Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys				
565	570	575	580	
caa gaa gcg gat gaa gag aaa cat ttg aat caa ggt gta aga aca tat				1830
Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val Arg Thr Tyr				
	585	590	595	

8 / 3 2

gtg gac ccc ttt acg tac gaa gat ccc aac caa gca gtg cga gag ttt 1878

Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe

600

605

610

gcc aaa gaa att gac gca tcc tgc att aag att gaa aaa gtt ata gga 1926

Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly

615

620

625

gtt ggt gaa ttt ggt gag gta tgc agt ggg cgt ctc aaa gtg cct ggc 1974

Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly

630

635

640

aag aga gag atc tgt gtg gct atc aag act ctg aaa gct ggt tat aca 2022

Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr

645

650

655

660

gac aaa cag agg aga gac ttc ctg agt gag gcc agc atc atg gga cag 2070

Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln

665

670

675

ttt gac cat ccg aac atc att cac ttg gaa ggc gtg gtc act aaa tgt 2118

Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Cys

680

685

690

aaa cca gta atg atc ata aca gag tac atg gag aat ggc tcc ttg gat 2166

Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp



9 / 3 2

695	700	705	
gca ttc ctc agg aaa aat gat ggc aga ttt aca gtc att cag ctg gtg 2214			
Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val			
710	715	720	
ggc atg ctt cgt ggc att ggg tct ggg atg aag tat tta tct gat atg 2262			
Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met			
725	730	735	740
agc tat gtg cat cgt gat ctg gcc gca cgg aac atc ctg gtg aac agc 2310			
Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser			
	745	750	755
aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc cga gtg ctt gag 2358			
Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu			
760	765	770	
gat gat ccg gaa gca gct tac acc acc agg ggt ggc aag att cct atc 2406			
Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile			
775	780	785	
cgg tgg act gcg cca gaa gca att gcc tat cgt aaa ttc aca tca gca 2454			
Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala			
790	795	800	

1 0 / 3 2

agt gat gta tgg agc tat gga atc gtt atg tgg gaa gtg atg tcg tac 2502  
 Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr  
 805 810 815 820

ggg gag agg ccc tat tgg gat atg tcc aat caa gat gtg att aaa gcc 2550  
 Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala  
 825 830 835

att gag gaa ggc tat cgg tta ccc cct cca atg gac tgc ccc att gcg 2598  
 Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala  
 840 845 850

ctc cac cag ctg atg cta gac tgc tgg cag aag gag agg agc gac agg 2646  
 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg  
 855 860 865

cct aaa ttt ggg cag att gtc aac atg ttg gac aaa ctc atc cgc aac 2694  
 Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn  
 870 875 880

ccc aac agc ttg aag agg aca ggg acg gag agc tcc aga cct aac act 2742  
 Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr  
 885 890 895 900

gcc ttg ttg gat cca agc tcc cct gaa ttc tct gct gtg gta tca gtg 2790  
 Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val

1 1 / 3 2

905	910	915	
ggc gat tgg ctc cag gcc att aaa atg gac cgg tat aag gat aac ttc			2838
Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe			
920	925	930	
aca gct gct ggt tat acc aca cta gag gct gtg gtg cac gtg aac cag			2886
Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln			
935	940	945	
gag gac ctg gca aga att ggt atc aca gcc atc acg cac cag aat aag			2934
Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys			
950	955	960	
att ttg agc agt gtc cag gca atg cga acc caa atg cag cag atg cac			2982
Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His			
965	970	975	980
ggc aga atg gtt ccc gtc tga gccagtactg aataaactca aaactcttga			3033
Gly Arg Met Val Pro Val			
985			
aattagttta cctcatccat gcactttaat tgaagaactg cacttttttt acttcgtctt			3093
cgccctctga aattaaagaa atgaaaaaaaa aaaacaatat ctgcagcggt gcttggtgca			3153
cagattgctg aaactgtggg gcttacagaa atgactgccg gtcatttgaa tgagacctgg			3213
aacaaatcgt ttctcagaag tactttttctg ttcatcacca gtctgtaaaa tacatgtacc			3273

1 2 / 3 2

tatagaaata gaacactgcc tctgagtttt gatgctgtat ttgctgccag acactgagct 3333  
 tctgagacat ccctgattct ctctccattt ggaattacaa ccattgtatt ttgtttgtgg 3393  
 cataaattac agtcatctgt ctttcactgg aatgaagacc atgcctagga acatttttta 3453  
 aggactcagc tgtgg 3468

&lt;210&gt; 2

&lt;211&gt; 986

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile

1

5

10

15

Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr

20

25

30

Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser

35

40

45

Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn

50

55

60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln

65

70

75

80

1 3 / 3 2

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg

85

90

95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro

100

105

110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu

115

120

125

Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys

130

135

140

Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly

145

150

155

160

Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu

165

170

175

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile

180

185

190

Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val

195

200

205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser

1 4 / 3 2

210	215	220
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys		
225	230	235 240
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro		
245	250	255
Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu		
260	265	270
Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala		
275	280	285
Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala		
290	295	300
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala		
305	310	315 320
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile		
325	330	335
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln		
340	345	350

1 5 / 3 2

Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys

355

360

365

Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val

370

375

380

His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile

385

390

395

400

Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val

405

410

415

Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val

420

425

430

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln

435

440

445

Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro

450

455

460

Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu

465

470

475

480

Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg

485

490

495

1 6 / 3 2

Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His

500

505

510

Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu

515

520

525

Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala

530

535

540

Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val

545

550

555

560

Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr

565

570

575

Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly

580

585

590

Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala

595

600

605

Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu

610

615

620

Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu



1 7 / 3 2

625                                  630                                  635                                  640

Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys

645                                  650                                  655

Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser

660                                  665                                  670

Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val

675                                  680                                  685

Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn

690                                  695                                  700

Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val

705                                  710                                  715                                  720

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr

725                                  730                                  735

Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile

740                                  745                                  750

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser

755                                  760                                  765

1 8 / 3 2

Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly  
770 775 780

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys  
785 790 795 800

Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu  
805 810 815

Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp  
820 825 830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp  
835 840 845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu  
850 855 860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys  
865 870 875 880

Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser  
885 890 895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala  
900 905 910

19 / 32

Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr

915

920

925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val

930

935

940

His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr

945

950

955

960

His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met

965

970

975

Gln Gln Met His Gly Arg Met Val Pro Val

980

985

&lt;210&gt; 3

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificial synthesized primer sequence for RT-PCR

&lt;400&gt; 3

20 / 32

gaaggcgtgg tcactaaatg taa

23

&lt;210&gt; 4

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificial synthesized primer sequence for RT-PCR

&lt;400&gt; 4

tttaatttca gagggcgaag ac

22

&lt;210&gt; 5

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificially synthesized primer sequence for RT-PCR

&lt;400&gt; 5

catccacgaa actaccttca act

23

2 1 / 3 2

&lt;210&gt; 6

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificially synthesized primer sequence for RT-PCR

&lt;400&gt; 6

tctccttaga gagaagtggg gtg

23

&lt;210&gt; 7

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificial synthesized primer sequence for RT-PCR

&lt;400&gt; 7

cacccccact gaaaaagaga

20

&lt;210&gt; 8

2 2 / 3 2

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificial synthesized primer sequence for RT-PCR

&lt;400&gt; 8

tacctgtgga gcaaggtgc

19

&lt;210&gt; 9

&lt;211&gt; 9

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificially synthesized spacer sequence for siRNA

&lt;400&gt; 9

ttcaagaga

9

&lt;210&gt; 10

&lt;211&gt; 19

&lt;212&gt; DNA

2 3 / 3 2

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificial synthesized target sequence for siRNA

&lt;400&gt; 10

gcagcaccat catccattg

19

&lt;210&gt; 11

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificial synthesized target sequence for siRNA

&lt;400&gt; 11

gaagcagcac gacttcttc

19

&lt;210&gt; 12

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial

2 4 / 3 2

&lt;220&gt;

&lt;223&gt; An artificially synthesized sequence for siRNA

&lt;400&gt; 12

caccgcagca ccatcatcca ttgttcaaga gacaatggat gatggtgctg c

51

&lt;210&gt; 13

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificially synthesized sequence for siRNA

&lt;400&gt; 13

aaaagcagca ccatcatcca ttgtctcttg aacaatggat gatggtgctg c

51

&lt;210&gt; 14

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; siRNA hairpin design



2 5 / 3 2

&lt;400&gt; 14

gcagcaccat catccattgt tcaagagaca atggatgatg gtgctgc

47

&lt;210&gt; 15

&lt;211&gt; 4863

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

<223> An artificially constructed plasmid sequence of siRNA expression vector.

&lt;400&gt; 15

gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctggat 60  
ccactagtaa cggccgccag tgtgctggaa ttcggcttgg ggatcagcgt ttgagtaaga 120  
gcccgcgtct gaacctccg cgccgccccg gcccagtgga aaagacgcgc aggcaaaacg 180  
caccacgtga cggagcgtga ccgcgcgccg agcgcgcgcc aaggtcgggc aggaagaggg 240  
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